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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/036,614ADATE: 03/01/1999
TIME: 14:09:33

INPUT SET: S30854.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information
4
5 (i) APPLICANT: Hillman, Jennifer L.
6 Lal, Preeti
7 Tang, Y. Tom
8 Yue, Henry
9 Corley, Neil C.
10
11 (ii) TITLE OF THE INVENTION: KINESIN LIGHT CHAIN HOMOLOG
12
13 (iii) NUMBER OF SEQUENCES: 3
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
17 (B) STREET: 3174 Porter Dr.
18 (C) CITY: Palo Alto
19 (D) STATE: CA
20 (E) COUNTRY: USA
21 (F) ZIP: 94304
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Diskette
25 (B) COMPUTER: IBM Compatible
26 (C) OPERATING SYSTEM: DOS
27 (D) SOFTWARE: FastSEQ for Windows Version 2.0
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: To Be Assigned
31 (B) FILING DATE: Filed Herewith
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER:
35 (B) FILING DATE:
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Billings, Lucy J.
39 (B) REGISTRATION NUMBER: 36,749
40 (C) REFERENCE/DOCKET NUMBER: PF-0484 US
41
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 650-855-0555
44 (B) TELEFAX: 650-845-4166
45
46 (2) INFORMATION FOR SEQ ID NO:1:

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47
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 619 amino acids
50          (B) TYPE: amino acid
51          (C) STRANDEDNESS: single
52          (D) TOPOLOGY: linear
53
54      (vii) IMMEDIATE SOURCE:
55          (A) LIBRARY: SMCANOT01
56          (B) CLONE: 2479739
57
58      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60      Met Ser Gly Leu Val Leu Gly Gln Arg Asp Glu Pro Ala Gly His Arg
61      1          5          10          15
62      Leu Ser Gln Glu Ile Leu Gly Ser Thr Arg Leu Val Ser Gln Gly
63      20          25          30
64      Leu Glu Ala Leu Arg Ser Glu His Gln Ala Val Leu Gln Ser Leu Ser
65      35          40          45
66      Gln Thr Ile Glu Cys Leu Gln Gln Gly Gly His Glu Glu Gly Leu Val
67      50          55          60
68      His Glu Lys Ala Arg Gln Leu Arg Arg Ser Met Glu Asn Ile Glu Leu
69      65          70          75          80
70      Gly Leu Ser Glu Ala Gln Val Met Leu Ala Leu Ala Ser His Leu Ser
71      85          90          95
72      Thr Val Glu Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu
73      100          105          110
74      Cys Gln Glu Asn Gln Trp Leu Arg Asp Glu Leu Ala Gly Thr Gln Gln
75      115          120          125
76      Arg Leu Gln Arg Ser Glu Gln Ala Val Ala Gln Leu Glu Glu Glu Lys
77      130          135          140
78      Lys His Leu Glu Phe Leu Gly Gln Leu Arg Gln Tyr Asp Glu Asp Gly
79      145          150          155          160
80      His Thr Ser Glu Glu Lys Glu Gly Asp Ala Thr Lys Asp Ser Leu Asp
81      165          170          175
82      Asp Leu Phe Pro Asn Glu Glu Glu Glu Asp Pro Ser Asn Gly Leu Ser
83      180          185          190
84      Arg Gly Gln Gly Ala Thr Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro
85      195          200          205
86      Ala Arg Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ala Gln
87      210          215          220
88      Gly Arg Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp
89      225          230          235          240
90      Leu Glu Arg Thr Ser Gly Arg Gly His Pro Asp Val Ala Thr Met Leu
91      245          250          255
92      Asn Ile Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Glu Ala
93      260          265          270
94      Ala His Leu Leu Asn Asp Ala Leu Ser Ile Arg Glu Ser Thr Leu Gly
95      275          280          285
96      Pro Asp His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu
97      290          295          300
98      Tyr Gly Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Gln Arg
99      305          310          315          320

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100  Ala Leu Glu Ile Arg Glu Lys Val Leu Gly Thr Asn His Pro Asp Val
101              325                      330                      335
102  Ala Lys Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys
103              340                      345                      350
104  Tyr Glu Ala Val Glu Arg Tyr Tyr Gln Arg Ala Leu Ala Ile Tyr Glu
105              355                      360                      365
106  Gly Gln Leu Gly Pro Asp Asn Pro Asn Val Ala Arg Thr Lys Asn Asn
107              370                      375                      380
108  Leu Ala Ser Cys Tyr Leu Lys Gln Gly Lys Tyr Ala Glu Ala Glu Thr
109              385                      390                      395                      400
110  Leu Tyr Lys Glu Ile Leu Thr Arg Ala His Val Gln Glu Phe Gly Ser
111              405                      410                      415
112  Val Asp Asp Asp His Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu
113              420                      425                      430
114  Glu Met Ser Lys Ser Arg His His Glu Gly Gly Thr Pro Tyr Ala Glu
115              435                      440                      445
116  Tyr Gly Gly Trp Tyr Lys Ala Cys Lys Val Ser Ser Pro Thr Val Asn
117              450                      455                      460
118  Thr Thr Leu Arg Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Leu
119              465                      470                      475                      480
120  Glu Ala Ala Glu Thr Leu Glu Glu Cys Ala Leu Arg Ser Arg Arg Gln
121              485                      490                      495
122  Gly Thr Asp Pro Ile Ser Gln Thr Lys Val Ala Glu Leu Leu Gly Glu
123              500                      505                      510
124  Ser Asp Gly Arg Arg Thr Ser Gln Glu Gly Pro Gly Asp Ser Val Lys
125              515                      520                      525
126  Phe Glu Gly Gly Glu Asp Ala Ser Val Ala Val Glu Trp Ser Gly Asp
127              530                      535                      540
128  Gly Ser Gly Thr Leu Gln Arg Ser Gly Ser Leu Gly Lys Ile Arg Asp
129              545                      550                      555                      560
130  Val Leu Arg Arg Ser Ser Glu Leu Leu Val Arg Lys Leu Gln Gly Thr
131              565                      570                      575
132  Glu Pro Arg Pro Ser Ser Ser Asn Met Lys Arg Ala Ala Ser Leu Asn
133              580                      585                      590
134  Tyr Leu Asn Gln Pro Ser Ala Ala Pro Leu Gln Val Ser Arg Gly Leu
135              595                      600                      605
136  Ser Ala Ser Thr Met Asp Leu Ser Ser Ser Ser
137              610                      615

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2453 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SMCANOT01

(B) CLONE: 2479739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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153	GTGAAGTGGT	GAAAGAAGGG	GTGGGAACGC	TGGACTTCTG	GACTTTGGGC	AGGGCAGATC	60
154	CTCTGACTCT	CTGGCTGCAG	AACAGTTTCT	TCCGTGCTCT	GGCCTGAGTG	CCCACAGGCC	120
155	AGGGGCCCTCT	GCTCTGTACA	CAGACCGGGC	AAGGTCCCCC	AGGCCAGGAT	GTCAGGCCTG	180
156	GTGTTGGGGC	AGCGGGATGA	GCCTGCAGGC	CACCGGCTCA	GCCAAGAGGA	GATCCTGGGG	240
157	AGCACACGGC	TGGTCAGCCA	AGGGCTAGAG	GCCCTACGCA	GTGAACACCA	GGCCGTGCTG	300
158	CAAAGCCTGT	CCCAGACCAT	TGAGTGTCTG	CAGCAGGGAG	GCCATGAGGA	AGGGCTGGTG	360
159	CATGAGAAGG	CCCGGCAGCT	TCGCCGTTCT	ATGGAAAACA	TTGAGCTCGG	GCTGAGTGAG	420
160	GCCCAGGTGA	TGCTGGCTCT	AGCCAGCCAC	CTGAGCACAG	TGGAGTCGGA	GAAACAGAAG	480
161	CTGCGGGCTC	AGGTGCGGCG	GCTATGCCAG	GAGAACCAGT	GGCTGCGGGA	TGAGCTGGCT	540
162	GGCACCCAGC	AGCGGCTACA	GCGCAGTGAA	CAGGCTGTGG	CTCAGCTGGA	GGAGGAAAAG	600
163	AAGCACCTGG	AGTTCTCTGG	GCAGCTGCGG	CAGTATGATG	AGGATGGACA	TACCTCGGAG	660
164	GAGAAAGAAG	GCGATGCCAC	CAAGGATTCC	CTGGATGACC	TCTTTCCTAA	TGAGGAGGAA	720
165	GAGGACCCCA	GCAATGGCTT	GTCCCGTGGT	CAAGGTGCTA	CAGCAGCTCA	GCAGGGTGGA	780
166	TATGAGATCC	CAGCAAGGTT	GCGGACGTTG	CACAACCTGG	TGATCCAGTA	CGCAGCCCAA	840
167	GGTCGCTATG	AGGTGGCCGT	GCCACTCTGT	AAGCAGGCAC	TAGAGGACCT	GGAGCGCACA	900
168	TCAGGCCGTG	GCCACCCTGA	TGTCGCCACC	ATGCTCAACA	TCCTTGCTTT	GGTGTATCGT	960
169	GACCAGAATA	AGTATAAGGA	AGCTGCCCAC	CTGCTGAATG	ATGCCCTTAG	CATCCGGGAG	1020
170	AGCACCTTGG	GACCTGACCA	TCCTGTCTGT	GCTGCCACAC	TCAACAATTT	GGCTGTGCTC	1080
171	TATGGCAAAA	GGGGCAAGTA	CAAGGAGGCA	GAGCCTCTGT	GCCAGCGGGC	ACTGGAGATT	1140
172	CGAGAAAAGG	TCCTGGGCAC	GAATCATCCA	GATGTGGCAA	AACAGCTGAA	CAACCTGGCC	1200
173	CTCTTGTGCC	AAAACCAGGG	CAAGTATGAG	GCCGTGGAAC	GCTACTACCA	GCGAGCACTG	1260
174	GCCATCTACG	AGGGGCAGCT	GGGGCCGGAC	AACCCTAATG	TAGCCCGGAC	CAAGAACAAC	1320
175	CTGGCTTCCT	GTTACCTGAA	ACAGGGCAAA	TATGCTGAGG	CTGAGACACT	ATACAAAGAG	1380
176	ATCCTGACCC	GTGCCCATGT	ACAGGAGTTT	GGGCTGTGG	ATGATGACCA	CAAGCCCATC	1440
177	TGGATGAAC	CAGAGGAGCG	GGAGGAAATG	AGCAAAAGCC	GGCACCATGA	GGGTGGGACA	1500
178	CCCTATGCTG	AGTATGGAGG	CTGGTACAAG	GCCTGCAAAG	TGAGCAGCCC	CACAGTGAAC	1560
179	ACTACTCTGA	GAAACCTGGG	AGCTCTGTAT	AGGCGCCAGG	GAAAGCTGGA	GGCTGCTGAG	1620
180	ACCCTGGAGG	AATGTGCCCT	GCGGTCCCGG	AGACAGGGCA	CTGACCCTAT	CAGCCAGACG	1680
181	AAGGTGSCAG	AGCTGCTTGG	GGAGAGTGAT	GGTAGAAGGA	CCTCCCAGGA	GGGCCCTGGA	1740
182	GACAGTGATG	AATTTCAGGG	TGGTGAAGAT	GCTTCTGTGG	CTGTGGAGTG	GTCCGGGGAT	1800
183	GGCAGTGGA	CCCTGCAGAG	GAGTGGCTCT	CTTGGCAAGA	TCCGGGATGT	GCTCCGCAGA	1860
184	AGCAGTGAAC	TCTTGGTGAG	GAAGCTCCAG	GGGACTGAGC	CTCGGCCCTC	CAGCAGCAAC	1920
185	ATGAAGCGAG	CAGCCTCCTT	GAACATCTCT	AACCAACCTA	GTGCAGCACC	CCTCCAGGTC	1980
186	TCCCGGGGCC	TCAGTGCCAG	CACCATGGAC	CTCTCTTCAA	GCAGCTGACA	TTCAACCCGG	2040
187	CCCCCAGGTC	TGCTGGGTCC	CCCCACCCCT	ACAGCCCTCA	CAGCATTTCC	CATTGCTCCT	2100
188	GGCTCTTCCC	CACCCCTAGG	TGGGACAGTG	AAGGGGAGCA	GTTTAACCAG	AAGATTGCTG	2160
189	CTGCCCTTAG	GGTCTCAGCT	CCCTCCTCAG	GAATCCCTCT	TAGGAAGGAC	CCTCAGGACA	2220
190	CCCTCTCTGC	ACCCTGTGGT	CCTCTAGAGT	AGCTAGCTCT	GAGGCCCAA	GGTGGGTACA	2280
191	AAGCAGGTAT	GGCCCTCAGA	GATGCAGCCT	GCTGTGGCT	TTTCAGTCAG	AGGGTTGGGG	2340
192	GCTGGCCAGC	CAAGCTGCCT	TGCCCTGGCC	GCTCTTACTC	CCTCCTCTCT	CTGTCTCACT	2400
193	TCAGGTCCAT	GTATTTCACT	TTTCTTAAAT	AAAAGAATCA	GTNCTTNTNT	NNG	2453

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 307085

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206
207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
208
209 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
210 1 5 10 15
211 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
212 20 25 30
213 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
214 35 40 45
215 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
216 50 55 60
217 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
218 65 70 75 80
219 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
220 85 90 95
221 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
222 100 105 110
223 Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
224 115 120 125
225 Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu
226 130 135 140
227 Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser
228 145 150 155 160
229 Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
230 165 170 175
231 Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
232 180 185 190
233 Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg
234 195 200 205
235 Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg
236 210 215 220
237 Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu
238 225 230 235 240
239 Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile
240 245 250 255
241 Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn
242 260 265 270
243 Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp
244 275 280 285
245 His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly
246 290 295 300
247 Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu
248 305 310 315 320
~~249 Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys~~
~~250 325 330 335~~
251 Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu
252 340 345 350
253 Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys
254 355 360 365
255 Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala
256 370 375 380
257 Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr
258 385 390 395 400

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/036,614A

DATE: 03/01/1999
TIME: 14:09:35

INPUT SET: S30854.raw

Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: To Be Assigned
